

GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 2645.71 seconds
(without alignments) 1579.326 Million cell updates/sec

Title: US-09-698-781-3

Perfect score: 1436

Sequence: 1MKQILHAALETTAATMLFPVLL.....KHOVLVRDCKASCNCNSIY 258

Scoring table: BLOSUM62

Xgapext 10.0 , Xgapext 0.5
Ygapext 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %
Listing first 45 summaries

Command line parameters:

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-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0_1 -LOOPCL=0 -IOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=15 -MODE=LOCAL
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-NO_XLXPY -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT=0
-WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Database :

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22: em_gss_fun: *
23: em_gss_main: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_poo: *
27: em_gss_rod: *

SUMMARIES

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3	943	65.7	1108	13	BM552843	BM552843 AGENCOURT
4	912	63.5	1063	13	BM55790	BM55790 AGENCOURT
5	869	60.5	803	13	BF897404	BF897404 IL2-MT018
6	867	60.4	450	12	BF897404	BF897404 IL2-MT018
7	867	60.4	808	13	BF897404	BF897404 IL2-MT018
8	858	59.7	462	12	BF897377	BF897377 IL2-MT018
9	858	59.7	781	13	BI82971	BI82971 603079842
10	850	59.2	464	12	BF89410	BF89410 IL2-MT018
11	830	57.8	451	12	BF89412	BF89412 IL2-MT018
12	825	57.5	443	12	BF897401	BF897401 IL2-MT018
13	823.5	57.3	904	13	BF897401	BF897401 603075145
14	814	56.7	420	12	BF897378	BF897378 IL2-MT018
15	814	56.7	784	13	BI825564	BI825564 603072524
16	807.5	56.2	946	13	BI832557	BI832557 603072889
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25	758	52.8	760	12	BG7232	BG7232 60265332
26	748	52.1	801	13	BI831850	BI831850 603078978
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30	737	51.3	730	13	BI559392	BI559392 603253072
31	736	51.3	721	13	BI830127	BI830127 603072754
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34	710.5	49.5	708	13	BI560558	BI560558 603254652
35	707	49.2	740	12	BG724382	BG724382 602652860
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37	706	49.2	401	12	BF897366	BF897366 IL2-MT018
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39	695.5	48.4	843	12	BG723588	BG723588 602654310
40	692.5	48.2	705	13	BI63698	BI63698 60306248
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42	679.5	47.3	849	13	BI562149	BI562149 60325338
43	669.9	46.9	600	10	BE58089	BE58089 169372
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45	670	46.7	870	13	BI465248	BI465248 603204748

ALIGNMENTS

RESULT 1

AL703262 LOCUS AL703262 DRKF2p686K DEFINITION mRNA linear EST 22-MAR-2002

ACCESSION DKEP686K1819_5', mRNA sequence.

VERSION AL703262.1 GI:19686617

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE (bases 1 to 547)

AUTHORS Poustka,A., Wellenreuther,R., Meves,H.W., Weil,B. and Wiemann,S.).

TITLE EST. (Poustka,A., Wellenreuther,R., Meves,H.W., Weil,B. and Wiemann

JOURNAL		S.)	
Unpublished (1999)		COMMENT	
Contact: Poustka A.J.			
Department Lehrach			
Max-Planck-Institute for Molecular Genetics			
Imrestrasse 73, 14195 Berlin, Germany			
Tel: +49-30-84131623			
Fax: +49-30-84131128			
Email: poustka@mpg-berlin-dahlem.mpg.de			
This is the 5' sequence of the clone insert.			
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer			
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;			
sequenced by DKFZ (German Cancer Research Center, Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.			
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/lab_host="DH10B"			
/note="Vector: ptriplex2; Site_1: SFI1; Site_2: SFI1B;			
CDNA-collection"			
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Best Local Similarity:	98.90%	N mismatches:	2
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	9	Gaps:	0
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AUTHORS			
NIH-MCC http://mcc.ncbi.nlm.nih.gov/			
TITLE			
National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL			
COMMENT			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cga@rsr@mail.nih.gov			
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Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			
Eukarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo;			
COMMENT			

Pred. No.: 1-44e-87
 Score: 867.00
 Percent Similarity: 81.98%
 Best Local Similarity: 73.42%
 Query Match: 60.38%
 DB: 13

QY 127 GluSerTrpAspGluTyrAsnAspPheAspGluValGlyProAspSerThrProAsn 146
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 OY 167 AsnAlaTrpCysProAspGlnLysValLeuValGlyLeuIleuProSerPhePro 186
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 122 CAAAGCTGTTGTTGATGAGTCAGTATGATTGTACTTGCGTAGGCCAAAGACTCCAAAC 181
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 147 AlaValValGlyHisTyrThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGly 166
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 Db 182 TCACTGGTGGGACATTACACGCTGTTGGTACTCTCATACCTGGATGGGA 241
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 167 AsnAlaTrpCysProAspGlnLysValLeuValGlyLeuIleuProSerPhePro 186
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 242 ATGGCTTACTGTGCCAATCAAAGATCTAAATACTACTATGTTGCCATATGTCCT 301
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 187 AlaGlyAsnTriPalaAsnArgLeuLeuValProTrpGluGlyAlaProCysAlaSer 206
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 302 GCTGGTAACTGGCTTAATGACTATGCTCTAAATACTACTATGTTGCCATATGTCCT 361
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 QY 207 CysProAspAspCysAspAspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTrp 226
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 362 TGCCGAGTAACTGAGATGACTATGCCACATGGTTCAGTACCAAAGATCTCTAT 421
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 227 SerAsnCysLysSerLeuLeuThr 235
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 Db 422 AGTAACTGTTAAAGTTGAGCTACA 448

RESULT 7

LOCUS B1826697 808 bp mRNA linear EST 04-OCT-2001
 DEFINITION Homo sapiens cDNA clone IMAGE:5169230 5',
 ACCESSION B1826697
 VERSION B1826697.1
 SOURCE
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgspps1@email.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: ILLM1420 row: n column: 15
 High quality sequence stop: 804.
 Location/Qualifiers
 1. .808
 /organism="Homo sapiens"
 /db_xref="IMAGE:5169230"
 /clone="IMAGE:5169230"
 /clone_id="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DHL10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; Note: Site 2: EcorI (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcorI site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
 BASE COUNT 248 a 187 c 170 g 203 t
 ORIGIN
 Alignment Scores:

RESULT 8

LOCUS BFO97377 462 bp mRNA linear EST 18-JAN-2001
 DEFINITION BFO97377-0181-201100-265-005 MT0181 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BFO97377
 VERSION BFO97377.1
 KEYWORD EST.
 SOURCE
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS 1 (bases 1 to 462)
 Dias Neto, E., Garcia Correa R., Verjovski-Almeida, S., Briones M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsumura, A., Bajaj, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Tondel, C., V. O'Farrell

QY 58 SHISASnGluLeuHgargArgAlaValSerProProAlaArgAsnMetLeuIysMetGluTr 78
 Db 302 ACACATGACTTACGAGAACGCTCTCCACCTCCAGTACCTGCTAAAGAGGATG 361
 QY 78 PASnlysGluAlaAlaAlaAsnAlaGlnlystPalaAsnGlnlysAsnTyRgHisse 98
 |:||||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||:
 Db 362 GAGCAGAGGAGGTACAACAGATGCCAACAGTGGCCAAAGTGCACTTACACATAG 421
 QY 98 IASnProLysPAsnGlyMetHsLeuIysCysGlyGluAsnLeuIysMetSerSerAl 118
 |:||||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 422 TGAATCCAGAGGACGGCAAAACCGATACAGATGTTGAGAACTCTATATGCACTGA 481
 QY 118 aProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluIysAsnAspPheAspH 138
 |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 482 CCCTRACTCTGCTTCGCTCCATCCAACTCCAACTGCTGAGCTGATTTGCTA 541
 QY 138 eGlyIglnGlyProIysThrProAsnAlaValAlaValAlaGlyHsTyrTrgIysValValTrpT 158
 |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 542 TGGCTGAGGACCCAAAGAGTCCCAAGTGCAGTTGCTGACATTAATCTCAGTTGTTGTA 601
 QY 158 rSerSerSerTrpIysValAlgIysGlyAsnAlaItyCysProAsnGlnlysValIysTr 178
 |:||||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 602 CTGGAATTACGGTAGGGATGCTACTGTCCTAAATCAGATGCTAAATA 661
 QY 178 rTyrTyValCysGlnTyCysProAlaGlyAsnTrpAlaAsnArgLeuTyValProTy 198
 |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 662 CTACTATGTTGCCATATGTTCTGCTGTTAATATGAAATAGAAATAGCA 721
 QY 198 rGluGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThr 217
 |:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 722 CCACAAAGGACACCTTGTCGCCGGTGCCTGTAAGCTGACAGAAAGCTATGCACC 779
 RESULT 10
 BFF97410
 LOCUS BFF97410 464 bp mRNA linear EST 18-JAN-2001
 DEFINITION mRNA sequence.
 ACCESSION MT0181 Homo sapiens cDNA, mRNA sequence.
 VERSION BFF97410.1 GI:12288856
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE BFF97410
 AUTHORS 1 (bases 1 to 464)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL2&l2=IL2-MT0181-281100-265-G04&t3=2000-11-28&t4=1>)
 Seq Primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 444.
 Location/Qualifiers 1..464
 source /organism="Homo sapiens"

 /db_xref="taxon:9606"
 /clone_id="MT0181"
 /dev_stage="Adult"
 /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 195,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription was performed under low mRNA and cDNA amplification conditions."
 BASE COUNT 144 a 96 c 98 g 123 t 3 others
 ORIGIN
 Alignment Scores:
 pred. No.: 4.93e-86 length: 464
 Score: 850.00 matches: 149
 Percent Similarity: 96.77% Conservative: 1
 Best Local Similarity: 96.13% Mismatches: 4
 Query Match: 59.19% Indels: 1
 DB: 12 Gaps: 0
 US-09-698-781-3 (1-258) x BFF97410 (1-464)
 QY 83 AlaAlaAsnAlaIglnlystPalaAsnGlyCysAsnTyRgHsSerAsnProlysAsp 102
 Db 2 GCAAGAAATGCCAAAGTGGCAACCCAGGCACTTACAGCTTACGATTCACAGGAT 61
 QY 103 ArgMetThrSerLeuIysCysGlyGluAsnLeuTyValProSerSerAlaProSerTrpT 122
 Db 62 CGAATGACAGCTCTAAATGTTGTTGAGATCTCTACATGTCAGTGCCTCCAGCTATCG 121
 QY 123 SerGlnAlaIleGlnSerTrpPheAspGluIysAsnAspPheAspPheGlyIvalGlyPro 142
 Db 122 TCACAGCACTCAAAAGCTGTTGATGACTACATGATGTTGACTTGTGAGGCCA 181
 QY 143 LysThrProAsnAlaValAlaValAlaGlyHsTyrTrgIysValValTrpTyrsSerTyru 162
 Db 182 AGACRCCCAACTCAGTGTGTTGAGATTAATACAGCTTACGATGTTGACTCTCACTC 241
 QY 163 ValGlyCysGlyAsnAlaItyCysProAsnGlnlysValLeuIysTrtyTrtyValCys 182
 Db 242 GTTGGATGTTGAAATGCTACTGTCCTAAATGCTTAC 301
 QY 183 GlnTrCysProAlaGlyAsnTrpAlaAsnArgLeuTyValProTyrgGlnGlyAla 202
 Db 302 CAATATGTTGCTGCGTGTAAATGGCTAAAGTACAGCTTATGCTTACACAAAGGCA 361
 QY 203 ProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCysLysTr 222
 Db 362 CCTTGCCAGTGGCCAGATACTGTCAGATGACTTACCCATGGTGCAGTAC 421
 QY 223 GluAspLeuTyTrsSerAsnCys-LysSerLeuIysLeuThrIeu 236
 Db 422 GAAGATCTCTATGTAATGCTAAAGNNTTGAGCTCACATTA 464
 RESULT 11
 BFF97412/C
 LOCUS BFF97412 451 bp mRNA linear EST 18-JAN-2001
 DEFINITION mRNA sequence.
 ACCESSION BFF97412
 VERSION BFF97412.1 GI:12288858
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	31	TGCAATTGTTCAACAGCATTAT	8
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br			
LOCUS	BF897401	443 bp	mRNA	linear EST 18-JAN-2001
DEFINITION	IL2-MT0181-281100-265-D11 MT0181 Homo sapiens CDNA, mRNA sequence.			
ACCESSION	BF897401			
VERSION	BF897401.1			
KEYWORDS	EST.			
SOURCE	human			
ORGANISM	Homo sapiens			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br			
REFERENCE	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0181-281100-265-G10&t3=2000-11-28&t4=1)			
AUTHORS	Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldman, G.H., Calvalho, A.F., Matsukuma, A., Bajaj, G.S., Simpson, D.H., Brusnelli, A., Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
BASE COUNT	130 a 94 c 92 g 131 t 4 others			
ORIGIN				
Alignment Scores:				
Pred. No.:	8.69e-84	Length:	451	
Score:	830.00	Matches:	144	
Percent Similarity:	97.97%	Conservative:	1	
Best Local Similarity:	97.30%	Mismatches:	3	
Query Match:	57.80%	Indels:	0	
DB:	12	Gaps:	0	
US-09-698-781-3 (1-258) x BF897412 (1-451)				
QY	111 HisGluAsnLeuThrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSerTrpHe	130		
Db	451 GAGATNCCTACATGTCAGTGCNNAGCTCATGGTCACAAGCAATCCAACCTGGTT	92		
QY	131 AspGluTyAsnAspPheAspPheGlyAlaGlyProlySthProAsnAlaValGly	150		
Db	391 GATGAGTACAGATGTTGACTTGGTAGGGCCAGAACCTCNCAACTCAGTGTGCA	332		
QY	151 HistYrrhGlyValValIrrpTySerSerTyLeuValGlyCysGlyAsnAlaTyrcys	170		
Db	331 CATTATACACAGGTTGTTGACTCTCATACCTCGTTGATGTTGAAATGCCTACTGT	272		
QY	171 ProAsnGlnLysValLeuLysTyrTyrTyValCysGlnTyrcysProAlaGlyAsnTrp	190		
Db	271 CCCCACATCAAAGAACTCTAAATTAACCTATGTTGCCAAATATGTCCTGTTAATTGG	212		
QY	191 AlaAsnArgAlaLeuThrValProTyGluGlnGlyAlaProCysAlaSerCysProAspAsn	210		
Db	211 GCTAAATAGACTATGTCCTATGCAACAGGACCACTTGCCAGTGCCAGTCAGATAC	152		
US-09-698-781-3 (1-258) x BF897401 (1-443)				
QY	211 CYSAspAspGlyIleauCysThrAspGlyCysLysLysTyrSerAsnCysLys	230		
Db	151 TGTGACGATGAGCTATGCAACATGGTGGAGTACGAGTCCTCATGTAATGCTAA	92		
QY	231 SerIleLeuIleuThrCysLysIleuValArgAspSerCysLysAlaSer	250		
Db	91 AGTTGAACTCACATTAACTGTTAACATCAGTGGTCAGGGACAGTGGCAAGGCCTC	32		
QY	251 CysAsnCysSerAsnSerIleTyr 258			

Qy 154 GlnvAlValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGln 173
 Db 322 CAGGTTGTTGTTGACTCTTCATACCGCGTGGATGGAAATGCCACTGCCAACTCAA 263

Qy 174 LysValLeuTyrTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTyrAlaAsnArg 193
 Db 262 AAAGTCTAAATACACTATGTTGCCATTATGCTGCTGGTAATGGCTATAGA 203

Qy 194 LeuTyrValProTyrGlyGluGlyAlaProCysAlaSerCysProAspCysAspASP 213
 Db 202 CTTATGTCCTTATGACAAGGAGCTTGCCAGTCCTGCTGGTAATGGCTATAGA 203

Qy 214 GlyLeuCysTyrAspGlyCysLysTyrGluLeuTyrSerAsnCysLysSerCys 233
 Db 142 GCACTATGCCAACATGTTGCAAGTAGGAGTCCTCATAGTACTGTTAAGTGTGA 83

Qy 234 LeuThrLeuTyrCysLysGlnLeuValArgAspSerCysLysAlaSerCysAsnCys 253
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Qy 254 SerAsnSerIleTyr 258
 Db 22 TCAAAGCAGTATT 8

RESULT 13
 B1830749

ACCESSION B1830749
 DEFINITION 60307515F1 NTH_MGC_119 Homo sapiens cDNA clone IMAGE:5167186 5', mRNA sequence.

VERSION B1830749.1
 KEYWORDS EST.

SOURCE human.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 904)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgsabst@nlm.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: ILM11415 Row: 1 column: 11
 High quality sequence stop: 827.

FEATURES source

1. .904 /organism="Homo sapiens"
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 /note="Organism: brain; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source: normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH-MGC Library."

BASE COUNT 278 a 201 c 193 g 232 t

ORIGIN Alignment Scores: 1.47e-82 Length: 904
 Pred. No.:

Score: 823.50
 Percent Similarity: 75.95%
 Best Local Similarity: 64.89%
 Query Match: 13
 DB: 13
 Gaps: 5

US-09-698-781-3 (1-258) x B1830749 (1-904)

Qy 1 MetLysGlnIleLeuHisProLeuLeuGluThr-----AlaMetThrLeuPhePr 18
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Qy 18 ovalLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLys 38
 Db 239 TCCGCCTTACTGCTGTTAACACCCAGTCAGTGCAAGTGCAAAGGGAGTTAA 298

Qy 185 GGTG--TTGTTCTGTTACTGTGCTGCTCTCCATCTTACCTGCA--GAGGAAGGA 238

Qy 38 PROAlaPheThrAlaLeuLeuLeuThrThrGlnThrGlnValGlnArgGluLeuValAsnLys 58
 Db 299 AGCAATGACTAAGGAGAGTCCTCCACTGCGCAGTACATCTAAGTGGATG 358

Qy 78 pasnLysGluAlaAlaAsnAlaGlnLysTpaAsnGinCysAsnTyrArgIle 98
 Db 359 GAGCAGAGAGGTACAAAGAATGCCAAAGGGGGCAACAGTGTCACTTACAACATAG 418

Qy 98 IAsnProLysAspArgMetThrSerIleLysCysGlyGluAsnLeuTyrMetSerSerAl 118
 Db 419 TGATCCAGGAGGCCAAACCGTACAGTCAGATGCTGGAGAACATCTATGTCAGTA 478

Qy 118 aproSerSerTyrSerSerGlnAlaIleGlnSerTyrPheAspGluTyrAsnAspPheAspPhe 138

Db 479 CCCTACTCTCCTGCTCTGCAATCCAAAGCTGGTGTAGGACATCTAGTGTCTA 537

Qy 138 eGlyValGlyProLysThrProAsnAlaValValGlyHisTyrGlnValValTrpTyr 158
 Db 598 CTCGACATACCGGTAGCTGGAAATGCCCAATCAGATGCTAAATA 657

Db 538 TGGTGTAGGACCAAAAGATGCCCAATGCGATTTGGACATTAACTCGAGCTGTTGGTA 597

Qy 158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuTyr 178

Db 599 CTCGACATACCGGTAGCTGGAAATGCCCAATCAGATGCTAAATA 657

Qy 178 TrpTyrValCysGlnTyrCysProAlaGlyAsnTyrAlaAsnArgLeuTyrValProT 198

Db 658 CTACTATGTTTCCCATATGTCGCTGGTGTGGTAATATGATAAGATAACCGT 717

Qy 198 YTGUGIUGIYAlaProCysAlaSerCysProAlaGlyAsnTyrAlaAsnArgLeuTyrValProT 198

Db 718 ACCAACAGGAAACACCTTGTCGGGTGCGCTGTGACTAAAGGACTATGTGCG 777

Qy 217 ThrasnGlyCysLysTyrGluAsp--LeuTyrSerAsnCysLysSerLeuLysLeuThr 236

Db 778 ACCAATAGTGTGCCAGTATCAGAAATCCTTAACTGTAATGTCAGTATCCTTGCAAGAAATT 837

Qy 236 euthrCys-----LysHisGlnLeuValArgAspSerCysLysAlaSerCys 251

Db 838 ACAGCTGGTGTGACACATGAGTACTCAGCGAAAGTGGCAGGTACTTGC 991

RESULT 14
 BF897378 BF897378
 LOCUS BF897378
 DEFINITION IL2-MT0181-281100-265-A06 MT0181 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF897378
 VERSION BF897378.1
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 420)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

QY	207	CysProAspAsnCysAspAspGlyLeuCysThrAspGlyCysLysTyrGlusIeu	225
Db	362	TCGCCAGATCTGTCAGATGGACTATGCCAAATGGTGCAGAGCAGATCTC	418
TITLE		Shotgun sequencing of the human transcriptome with ORF expressed	
JOURNAL		sequence tags	
COMMENT		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
MEDLINE	20202663	Contact: Simpson A.J.G.	
CONTACT		Ludwig Institute for Cancer Genetics	
Laboratory		Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	
TELEPHONE		Tel: +55-11-2704922	
FAX		Fax: +55-11-2707001	
EMAIL		asimpson@ludwig.org.br	
SEQUENCE		This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0181-281100-655-A00873=2000-11-28&t4=1)	
SEQ_PRIMER		Seq primer: puc 18 forward	
FEATURES		High quality sequence stop: 397.	
source		location/Qualifiers	
DB:	420	1. /organism="Homo sapiens"	
BASE COUNT		/db_xref="taxon:9606"	
ORIGIN		/clone_id="MT0181"	
FEATURES		/dev_stage="Adult"	
source		/note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
DB:	127	a 90 c 91 g 112 t	
BASE COUNT		Alignment Scores:	
ORIGIN		Pred. No.: 5.03e-82	
FEATURES		Score: 84.00	
source		Percent Similarity: 100.00%	
DB:		Best Local Similarity: 99.28%	
BASE COUNT		Query Match: 56.69%	
ORIGIN		DB: 12	
FEATURES		Gaps: 0	
source		Alignment Scores:	
DB:	87	Pred. No.: 5.03e-82	
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FEATURES		Best Local Similarity: 99.28%	
source		Query Match: 56.69%	
DB:	2	Gaps: 0	
BASE COUNT		US-09-698-781-3 (1-258) x B897378 (1-420)	
ORIGIN		Alignment Scores:	
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ORIGIN		Percent Similarity: 100.00%	
FEATURES		Best Local Similarity: 99.28%	
source		Query Match: 56.69%	
DB:	107	Gaps: 0	
BASE COUNT		US-09-698-781-3 (1-258) x B1825564 (1-784)	
ORIGIN		Alignment Scores:	
DB:	62	Pred. No.: 5.03e-82	
BASE COUNT		Score: 84.00	
ORIGIN		Percent Similarity: 100.00%	
FEATURES		Best Local Similarity: 99.28%	
source		Query Match: 56.69%	
DB:	122	Gaps: 0	
BASE COUNT		US-09-698-781-3 (1-258) x B1825564 (1-784)	
ORIGIN		Alignment Scores:	
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BASE COUNT		Score: 84.00	
ORIGIN		Percent Similarity: 100.00%	
FEATURES		Best Local Similarity: 99.28%	
source		Query Match: 56.69%	
DB:	167	Gaps: 0	
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source		Query Match: 56.69%	
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BASE COUNT		US-09-698-781-3 (1-258) x B1825564 (1-784)	
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ORIGIN		Percent Similarity: 100.00%	
FEATURES		Best Local Similarity: 99.28%	
source		Query Match: 56.69%	
DB:	309	Gaps: 0	

QY 58 LysHisAsnGlueuArgArgGalaValSerProProAlaArgAsnMetLeuLysMetGlu 77
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 310 AACACAATGAACTAGAAAGCAGTCCTCAGCTGCCAGTAAAGATGGAA 369
 QY 78 TrpAsnLysGluAlaAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTy-ArgHis 97
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 370 TGGAGCAGAGGAGGTAAACACGAAATGCCAAAGGGCAACAGTCAGTGCACCTTACACAT 429
 QY 98 SerAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTy-MetSer 117
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 430 ATGATCCAGAGCGAACACAGTACAGATCTGGTACAGATCTCTATATGTCAGT 489
 QY 118 AlaProSerSerTpsergInalAlaLegInserPheAspGluTyrosAspPheAsp 137
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 Db 490 GACCTACTTCTGCTCTGCAATCCAAAGCTGGTATGACGAGATCTTAGATTTGRC 549
 QY 138 PheGlyValGlyProLysThrProAsnAlaValAlaValGly-HisTyThrGlnValValPhe 157
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 QY 158 TyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrcySProAsnGlnLysValLeuLys 177
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 QY 178 TyrTyTyTyValCysGlnTyrcySProAlaGlyAsnTrpAlaAsnArgLeuTy-ValPro 197
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 Db 670 TACTACTATTTGCCAATATGTCCTGCTGGTAAATAATGAAATAGAAATAGAAATACCCCG 729
 QY 198 TyrGluGlyAlaProCysAla-SerCysProAspAspCysAspAspGlyLeu 215
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Search completed: March 14, 2003, 05:26:15

Job time : 2648.71 secs